

CRFI



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/827,498

DATE: 09/08/2004

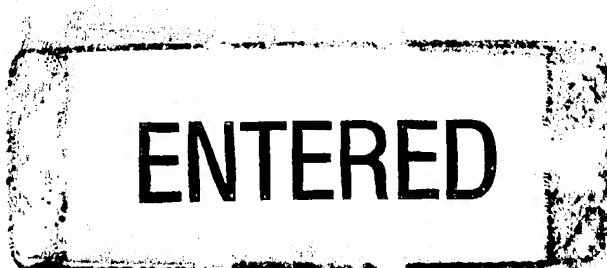
TIME: 13:57:55

Input Set : N:\efs\10827498\AMBI1001.txt

Output Set: N:\CRF4\09082004\J827498.raw

3 <110> APPLICANT: Ambion, Inc.
 4 Chen, Lianling
 5 Setterquist, Robert
 6 Latham, Gary
 8 <120> TITLE OF INVENTION: Recombinant Reverse Transcriptases
 10 <130> FILE REFERENCE: AMBI:1001
 12 <140> CURRENT APPLICATION NUMBER: 10/827,498
 C--> 13 <141> CURRENT FILING DATE: 2004-04-19
 15 <160> NUMBER OF SEQ ID NOS: 20
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2037
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Moloney murine sarcoma virus
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(2037)
 29 <400> SEQUENCE: 1

30 atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa	48
31 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys	
32 1 5 10 15	
34 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag	96
35 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln	
36 20 25 30	
38 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct	144
39 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro	
40 35 40 45	
42 ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa	192
43 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln	
44 50 55 60	
46 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag	240
47 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln	
48 65 70 75 80	
50 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac	288
51 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn	
52 85 90 95	
54 acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct	336
55 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro	
56 100 105 110	
58 gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc	384
59 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro	
60 115 120 125	
62 acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc cca ccg tcc cac	432



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63	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
64		130					135					140					
66	cag	tgg	tac	act	gtg	ctt	gat	tta	aag	gat	gcc	tat	ttc	tgc	ctg	aga	480
67	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Tyr	Phe	Cys	Leu	Arg	
68	145					150					155					160	
70	ctc	cac	ccc	acc	agt	cag	cct	ctc	ttc	gcc	ttt	gag	tgg	aga	gat	cca	528
71	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
72						165					170					175	
74	gag	atg	gga	atc	tca	gga	caa	ttg	acc	tgg	acc	aga	ctc	cca	cag	ggt	576
75	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	Leu	Pro	Gln	Gly	
76				180						185					190		
78	ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	cac	aga	gac	cta	624
79	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	His	Arg	Asp	Leu	
80			195						200					205			
82	gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	cta	cag	tac	gtg	672
83	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	Leu	Gln	Tyr	Val	
84		210					215					220					
86	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	tgc	caa	caa	ggt	720
87	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	Cys	Gln	Gln	Gly	
88	225					230					235					240	
90	act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	tat	cgg	gcc	tcg	768
91	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly	Tyr	Arg	Ala	Ser	
92					245					250					255		
94	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	tat	ctg	ggg	tat	816
95	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	Tyr	Leu	Gly	Tyr	
96			260						265					270			
98	ctt	cta	aaa	gag	ggt	cag	aga	tgg	ctg	act	gag	gcc	aga	aaa	gag	act	864
99	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	Arg	Lys	Glu	Thr	
100			275						280					285			
102	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	cta	agg	gag	ttc	912
103	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe	
104		290						295				300					
106	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	ggg	ttt	gca	gaa	960
107	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	Gly	Phe	Ala	Glu	
108	305					310					315					320	
110	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	act	ctg	ttt	aat	1008
111	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	Thr	Leu	Phe	Asn	
112					325					330					335		
114	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	aag	caa	gct	ctt	1056
115	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	Lys	Gln	Ala	Leu	
116			340						345					350			
118	cta	act	gcc	cca	gcc	ctg	ggg	ttg	cca	gat	ttg	act	aag	ccc	ttt	gaa	1104
119	Leu	Thr	Ala	Pro	Ala	Leu	Gly	Leu	Pro	Asp	Leu	Thr	Lys	Pro	Phe	Glu	
120			355					360						365			
122	ctc	ttt	gtc	gac	gag	aag	cag	ggc	tac	gcc	aaa	ggt	gtc	cta	acg	caa	1152
123	Leu	Phe	Val	Asp	Glu	Lys	Gln	Gly	Tyr	Ala	Lys	Gly	Val	Leu	Thr	Gln	
124		370					375					380					
126	aaa	ctg	gga	cct	tgg	cgt	cgg	ccg	gtg	gcc	tac	ctg	tcc	aaa	aag	cta	1200
127	Lys	Leu	Gly	Pro	Trp	Arg	Arg	Pro	Val	Ala	Tyr	Leu	Ser	Lys	Lys	Leu	

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128	385		390		395		400	
130	gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc							1248
131	Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala							
132		405		410		415		
134	att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca							1296
135	Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro							
136		420		425		430		
138	cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc							1344
139	Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro							
140		435		440		445		
142	ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg							1392
143	Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu							
144		450		455		460		
146	ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac							1440
147	Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn							
148	465		470		475		480	
150	ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg caa cac aac tgc							1488
151	Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys							
152		485		490		495		
154	ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac							1536
155	Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp							
156		500		505		510		
158	cag ccg ctc cca gac gcc gac cac acc tgg tac acg gat gga agc agt							1584
159	Gln Pro Leu Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Asp Gly Ser Ser							
160		515		520		525		
162	ctc tta caa gag gga cag cgt aag gcg gga gct gcg gtg acc acc gag							1632
163	Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Val Thr Thr Glu							
164		530		535		540		
166	acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag							1680
167	Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln							
168	545		550		555		560	
170	cgg gct gaa ctg ata gca ctc acc cag gcc cta aag atg gca gaa ggt							1728
171	Arg Ala Glu Leu Ile Ala Leu Thr Gln Ala Leu Lys Met Ala Glu Gly							
172		565		570		575		
174	aag aag cta aat gtt tat act gat agc cgt tat gct ttt gct act gcc							1776
175	Lys Lys Leu Asn Val Tyr Thr Asp Ser Arg Tyr Ala Phe Ala Thr Ala							
176		580		585		590		
178	cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa							1824
179	His Ile His Gly Glu Ile Tyr Arg Arg Gly Leu Leu Thr Ser Glu							
180		595		600		605		
182	ggc aaa gag atc aaa aat aaa gac gag atc ttg gcc cta cta aaa gcc							1872
183	Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala							
184		610		615		620		
186	ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt ccc ggg ggt caa							1920
187	Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly Gly Gln							
188	625		630		635		640	
190	aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg							1968
191	Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala							
192		645		650		655		

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194 gcc cga aag gca gcc atc aca gag act cca gac acc tct acc ctc ctc      2016
195 Ala Arg Lys Ala Ala Ile Thr Glu Thr Pro Asp Thr Ser Thr Leu Leu
196          660          665          670
198 cac cac cac cac cac taa
199 His His His His His
200          675
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 678
205 <212> TYPE: PRT
206 <213> ORGANISM: Moloney murine sarcoma virus
208 <400> SEQUENCE: 2
210 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
211 1          5          10          15
214 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
215          20          25          30
218 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
219          35          40          45
222 Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
223          50          55          60
226 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
227 65          70          75          80
230 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
231          85          90          95
234 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
235          100          105          110
238 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
239          115          120          125
242 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
243          130          135          140
246 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Tyr Phe Cys Leu Arg
247 145          150          155          160
250 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
251          165          170          175
254 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
255          180          185          190
258 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu
259          195          200          205
262 Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
263          210          215          220
266 Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
267 225          230          235          240
270 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser
271          245          250          255
274 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
275          260          265          270
278 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
279          275          280          285
282 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
283          290          295          300

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286 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
287 305          310          315          320
290 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
291          325          330          335
294 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
295          340          345          350
298 Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
299          355          360          365
302 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
303          370          375          380
306 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
307 385          390          395          400
310 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
311          405          410          415
314 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
315          420          425          430
318 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
319          435          440          445
322 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
323          450          455          460
326 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
327 465          470          475          480
330 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
331          485          490          495
334 Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
335          500          505          510
338 Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Asp Gly Ser Ser
339          515          520          525
342 Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
343          530          535          540
346 Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
347 545          550          555          560
350 Arg Ala Glu Leu Ile Ala Leu Thr Gln Ala Leu Lys Met Ala Glu Gly
351          565          570          575
354 Lys Lys Leu Asn Val Tyr Thr Asp Ser Arg Tyr Ala Phe Ala Thr Ala
355          580          585          590
358 His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu
359          595          600          605
362 Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
363          610          615          620
366 Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly Gly Gln
367 625          630          635          640
370 Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
371          645          650          655
374 Ala Arg Lys Ala Ala Ile Thr Glu Thr Pro Asp Thr Ser Thr Leu Leu
375          660          665          670
378 His His His His His His
379          675
382 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\efs\10827498\AMBI1001.txt

Output Set: N:\CRF4\09082004\J827498.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20

VERIFICATION SUMMARY

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Input Set : N:\efs\10827498\AMBI1001.txt

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date